

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 23:03:11 ; Search time 1328.9 Seconds

(without alignments)
921.325 Million cell updates/sec

Title: US-10-043-573-57

Sequence: 1 TCCTTACGCGCTTCAAGCGCA.....CGGCTGGCTCATGGGTGCC 41

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estmu: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estum: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_huv: *
19: em_gss_pln: *
20: em_gss_vit: *
21: em_gss_fun: *
22: em_gss_man: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rtd: *
26: em_gss_pig: *
27: em_gss_vil: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	418	28	BZ513765 BOMQF58TF
2	39	95.1	554	12	BG543860 E1595 CH1
3	39	95.1	609	14	CD836743 BN45_049M
4	39	95.1	692	28	BZ026652 CE154H01

5	39	95.1	695	14	CD836545
6	39	95.1	729	14	CD837127
7	37.4	91.2	510	9	AV525264
8	37.4	91.2	519	14	T43079
9	37.4	91.2	679	9	AV823338
10	37.4	91.2	681	13	BH636585
11	35.8	87.3	844	28	BH679886
12	34.8	84.9	400	14	T41914
13	34.2	83.4	592	28	BZ452017
14	32.6	79.5	237	28	BZ662189
15	32.6	79.5	373	28	BH813089
16	32.6	79.5	574	9	AU239055
17	31	75.6	155	28	BH813082
18	28.6	69.8	554	12	BH563044
19	27.4	66.8	477	9	AV409658
20	27.4	66.8	498	12	B1417863
21	27.4	66.8	634	10	AW720138
22	27.4	66.8	670	10	AW720608
23	25.8	62.9	278	9	AV409319
24	24.8	60.5	646	14	CF450636
25	24.6	60.0	415	28	BH214235
26	24.6	60.0	494	9	AV525554
27	24.4	59.5	594	14	CB429996
28	24.4	59.5	642	14	CB445689
29	23.8	58.0	766	14	CB937022
30	23.8	58.0	786	12	BQ126292
31	23.6	57.6	363	29	CG360855
32	23.6	57.6	369	28	BZ014648
33	23.4	57.1	628	14	CA483454
34	23.4	57.1	722	29	CE096697
35	23	56.1	293	10	BH511371
36	23	56.1	428	14	N32472
37	23	56.1	907	10	BE782561
38	22.8	55.6	162	28	AZ889138
39	22.8	55.6	683	14	CB453647
40	22.8	55.6	769	29	CG349119
41	22.8	55.6	954	29	CG352400
42	22.6	55.1	421	28	AQ034106
43	22.6	55.1	547	12	BH330357
44	22.6	55.1	577	12	BQ000834
45	22.6	55.1	578	9	AJ457247

ALIGNMENTS

RESULT 1
LOCUS BZ513765/c
DEFINITION BOMQF58TF BO_2.3 KB Brassica oleracea genomic clone BOMQF58,
genomic survey sequence.
ACCESSION BZ513765
VERSION BZ513765.1 GI:27040986
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 418)
Town, C.D., Van Aken, S., Uteerback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSS: BOMQF58TF
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.